

Approximate distance from p telomere (Mb)

7.60

7.75

D19S1184

D19S1186

KIAA0521

MG-4

MG-12

MG-1

MG-2

NTE

R31913

BC672420

BC903416

MUCL4 genomic structure

exons

mg2-GWF4

mg2-EF4

mg2-ER4

mg2-ER6

AJ deletion

1 2 3 4 5 6 7 8 9 10 11 12

1314

bps

1

13270

Transcript map

Physical Map

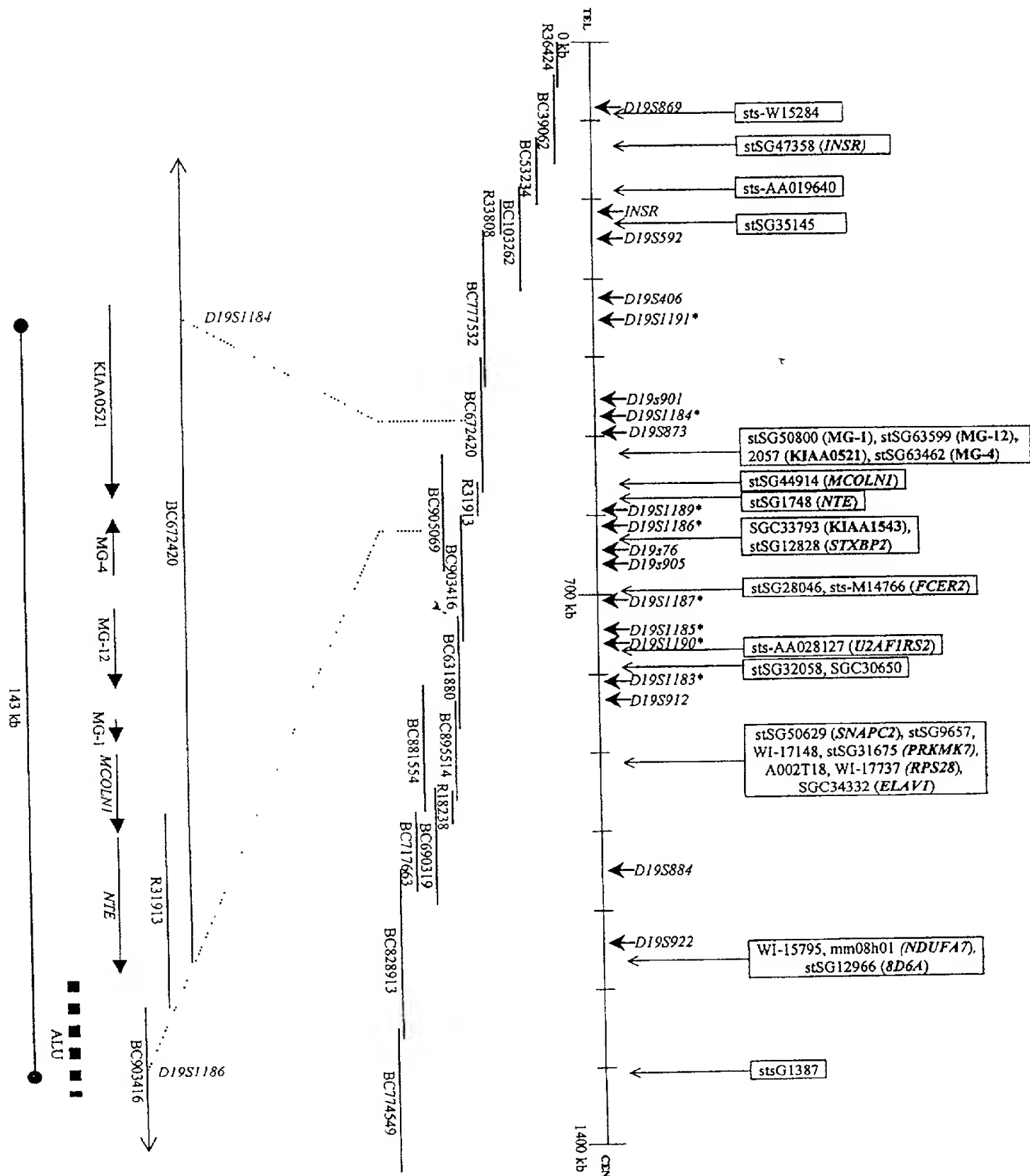


Fig. 1B

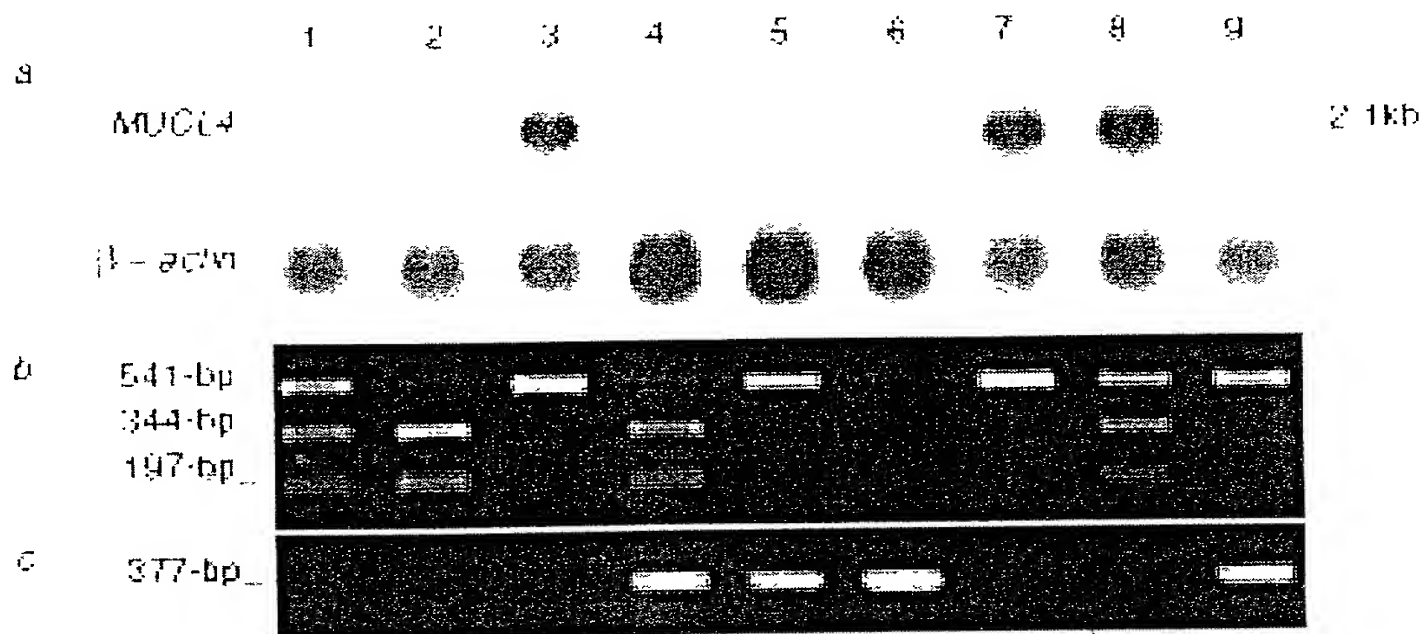


FIGURE 2

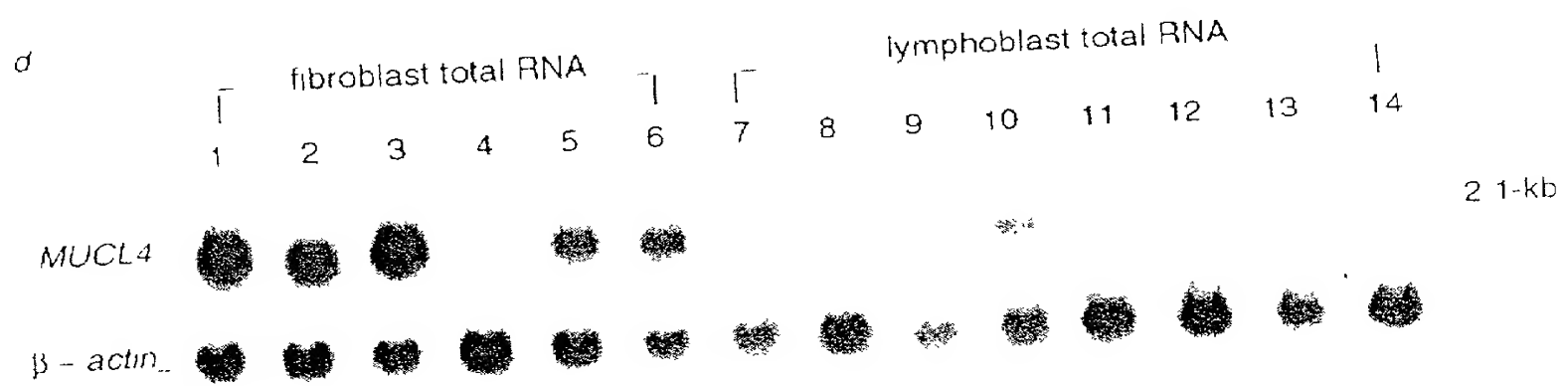


Figure 2

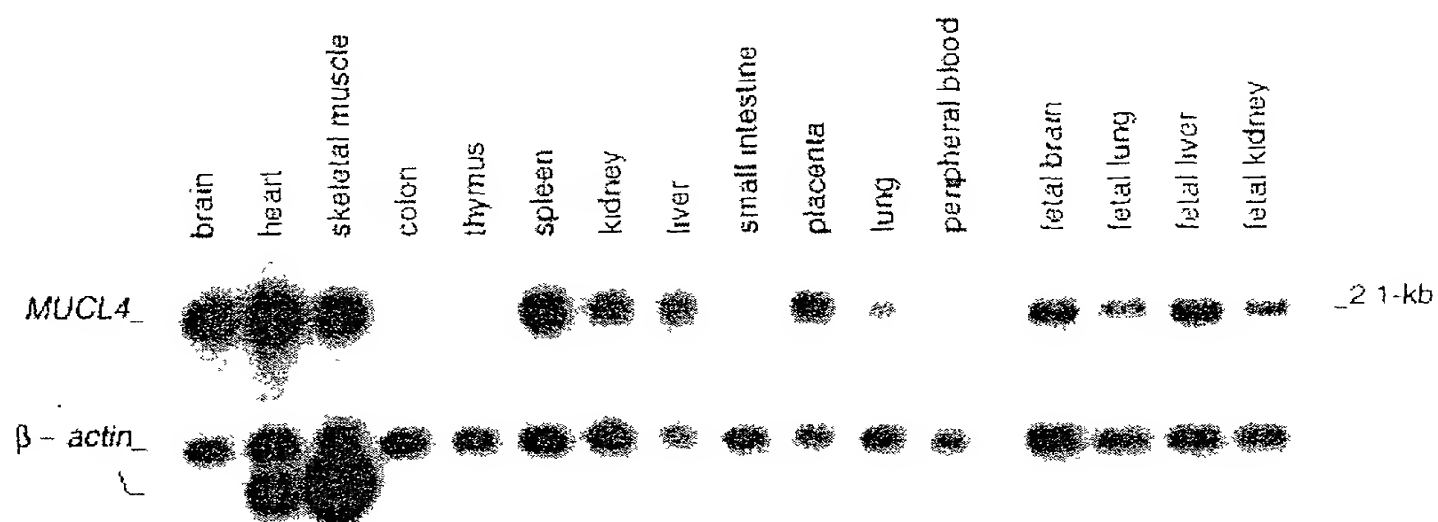


FIGURE 3

1. MTAPAGPRGSEERLLTNPCTGTAQSPSP...APPTPEEDERRKIK
1. MADPEVVVCSSSHENRCNENQOTSPS...EELLLEDMRRKIK
1MQSYGPGAQTAPVKRRTDSYEAQQQQQSPESDEEYVNTRIILRRVQLQSTFVAVPEPISAGSGTAPPSVDGREEQEFPGSSAASYQEERMRKIQ

47 FEMSPCKERAKGRPKM QVVKIL VVTL FGLSNQAVT EREENTIAFHLFLGYS DG...ADDTFAAYTR EQYQAEFAHVDQYLA
44 FEMNPCKEKEWARGKPKIA QIKLIA VVTL FGLSNQ VVAEKEENTIAFHLFLGYS DR...MODDTFAAYTOSD YDQ I EAVNOYL
101 FEMNPIEKQAKRKEPKF QIVKIF VVTL CLFAHGRYNHNYTGNREAFSHLELRGNDSSREVESYPPEVGPFA YLXSEFDT QAVNGYAN

139 LPDVSGRYAVRGGCDPWTCNGSCALCQRYERGHVDEANDTEDIDPMVTD CIOVDPPEPPPPPSDDLT EESSSYNLTIKFKHLVNVTHERLKK
136 LYNVSVGNHAYENKG...TKQSAVA COHAYKRCNIMPCNDTEDIDPEIETOCFEVEDE...P...FHGCTPAENKUNLTLDEHRLAVELOEKLKK
200 SRSIGPYDPTPN...NTMPPKICLONRECTI GENESMIEDPHIDEVCERPEPNT...TICVENYLRODVEENFASLVSQOLTEKIK

239 TINLOSIN NE PDCYTESAL TJEDNKAHSCRIPISLETOAHIOECK...HPSVEQHCDNSERLFFDVVILTCSLSELCARSLRGILLONEEVGCH
224 AINLOVRH CEPDCYDE TTEFNKAHSGRIKISLNDI ISHRECKDW HVSGSIKNHMMEDAEVILTCI SLICIRS RGLQLOQEEVNFVE
287 TNEKANGGLSAPDCEREDUSITENNRDEDGOML SLDAAFAIRLKCHGATDFISDANFDNMLRSYINFEVLTCAI SEALCTRALWRVLLRCTTVNE

335 WRQRCVSIWRLFEVNGWYIIVTSDVLTISCTIKK CLEAKNTAS...YDVCSILLGTSTLLVMGVIRYLTEFNHYNLTLATLSVALPSVARECC
322 LHKKEYSVSOEFVNGWYIMII ISDLTILIGSILKEIOAKSLTS...YDVCSILLGTSTLLVMGVIRYIGFFAKYNLITLLOALPNVRFCCCK
387 RSQCKESFDGRLEFVNGWYIMII FNDVLTIGSALKEQIECRYLVVDQWDTCSFELGIGNLLVFGVIRYIGFFAKYNLITLLOALPNVRFCCCK

433 AIVLYGCFCCGNI VLGPIH KERSLSMVSECLFSLINGDDMEVTFAMQAQQCRSSLLVWLFSEQYLYSFISLFTYVMSLFLIALITCAYDTIKHPGCAC
420 AIVLYGCFCCGNI VLGPIH KERSLSMVSECLFSLINGDDMEFATFAMQO...KSYLVWLFSTRYLYSFISLFTYVMSLFLIALITDITYTIKQYQDQCG
487 LLYAGVECCMILGPYH KERSLATTSECLFALINGDDMEFATFATISS...KAWWVWFEQYLYSFISLFTYVMSLFLIALITDITYTIKQYQDQCG

533 ESELOAVIACQ DSPSGKERRGSG...SACSLCCCCGRDPSEHSLVN...
517 PETELRTEISECK DLPNSCKRLDD...PPVSLFCCCKK...
584 PTTDLKARVGTRTANDISGVEMTLDDEDQTSFLDVVKS CCCCGRGHRQEPAPQNSGYTSLSSIMK

Figure 4A

